

Human 23565

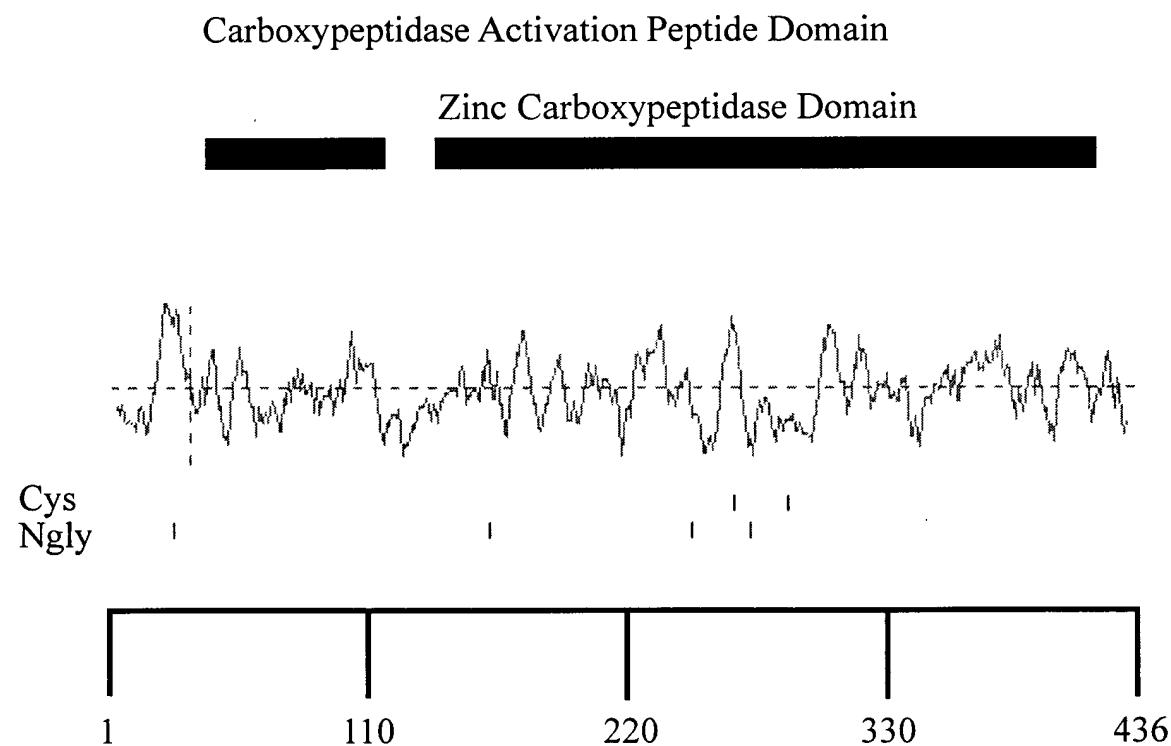


Fig. 1

Zn_carbOpept: domain 1 of 1, from 139 to 419; score 413.7, E = 1.7e-120

* ->Yhnleeiyaw1D11vsnfPdLvsksvsiGksyeGRd1kvlKisdnpat
 Yh+leeiy+w+D+ v ++ d+vsks+ig+s+e+ + vLK+s++
 Fbh23565f1 139 YHTLEEIYSWIDNFVMEHSIDIVSKIQIGNSFENQSILVLFSTG--- 182
 genePevfavagwiHAREwvtsAt11w11kelvanYgsDktitk11dg1d
 g++ P+++++g iH+REW+t At w+++++v+++Yg D t++1+ +d
 Fbh23565f1 183 GSRHPAIWIDTG- IHSREWITHTAGIWTANKIVSDYKGDRVLTIDLNAMD 231
 1fy1lpvfnpDGYaYsitttSYRmWRKtRspnagsfcvGtDpNRNWyaqw
 ++i v+NpDG+a+++ + R+WRK+ s ++g fc+G+D+NRNW +++
 Fbh23565f1 232 -IFIELVTNPDGFIAFTHSMN - RLIWRKKNKSIRPGIFCIGVDLNRNWKSGF 278-
 ggmgassysPcSetYegTapsSepEtkaVedfirsw1ggGkqnIkayItf
 gg g +s +PcSetY+G+ p Se E+ +a+++fi + + n ka+I++
 Fbh23565f1 279 GGNGSNS-NPCSETYHGPSPQSESEVAIAVNFITAHG----NFKALISI 322
 HsYSQL11YPYgydyn1npdand1de1s1kiaadalsarhgtYyt1g1P
 HsYsq+1+YPYg+ + + +1 +1+ k a+ a1 hg y g +
 Fbh23565f1 323 HSYSQMLMYPYGRLLEPVSNQRELYDLA--KDAVEALYKVHGEYIFG-S 369
 gsstIYpasAGGsdDwaydvgiikyaff fE1rlrpdtgsyGnPcF11PeeqI
 +s+t+Y+as G + Dwayd g ikyaf fE1r dtg yg F11P+qI
 Fbh23565f1 370 ISTTLYVAS-GITVWDWAYDSG- IKYAFSFELR-DTGGQYG--FLLPATQI 413
 iptgsee<-* (SEQ ID NO: 4)
 Fbh23565f1 414 IPTAQ-E 419

Fig. 2A

zn_carb: domain 1 of 1, from 139 to 419; score 401.8, E = 6.7e-117

* ->Yhsyeeinaw1ddLarnyPd1tsVsliSiGksyeGRpiKvLki . . .
 Yh++eei++w+d+ +++ d+ Vs i+ig+s+e+ i+vLk+++++
 Fbh23565f1 139 YHTLLEEIYSWIDNFVMEHSDI --VSKIQIGNSFENQSI1VLKFstgg 183
 . . .kpavfidagiHAREWiapatalylinqLltneteySkdpddegsvtkl
 ++ pa++id giH REWi+ at ++n+++++ Y+kd ++ t++
 Fbh23565f1 184 srHPAlWIDTGIHSREWITHATGIWTANKIVSD---YGKD-RV---LTDI 226
 Ldk1dwyiPvwmNPDGYeythtsdR1WRKnsPngasgsqgtwyncyGv
 L+ +d++i v+NPDG++th+ ++R1WRKn s + C+GV
 Fbh23565f1 227 LNAMDFIELVNTNPDGFAFTHS -MNRLWRKNSIRPG----IF-CIGV 268
 D1NRNFdfhnWgeigGssslpcsetyAGsspfSeWEpEtkalldfilsne
 D1NRN+ ++ +g+ Gs+s+pcsety+G+sp+S E E+ a+ +fi+ +
 Fbh23565f1 269 DLNRNWKG-FGGN-GSNSNPSETYHGPSPQS--ESEVAAIVNFIATAH- 313
 igkgrikayis1Hsysq111YPyGytnatvppngdlhkevakaakaig
 g+ka is+Hsysq+1+YPyG + +n+++1 ++ak a++a+
 Fbh23565f1 314 --GNFKALISIHSYSQMLMYPYGRLL-EPVSNQRELY-DLAKDAVEALY 358
 dyyfggt1YtpGssssadpd1dit1YpassGssdDwaygt1kgvkystyIEL
 +++ G Y G s+++ t1Y asG++ Dway+ + +ky++ +EL
 Fbh23565f1 359 KVH--GIEYIFG-SIST----TLYVASGITVDAYDSG--IKYAFSFEL 398
 rdtgddagrygF1LppscvkpvrmegriptgeE<-* (SEQ ID NO: 5)
 rdt g+ygF1Lp+ qipt+ E
 Fbh23565f1 399 RDT----GQYGFLLPA----TQIIPTAQE 419

Fig. 2B

Propep_M14: domain 1 of 1, from 41 to 118: score 100.3, E = 3.8e-26

* ->qV1rvkvadedQvk11kdLentehleDFwkpdsatpikpqstvDfr
qV1rv + de+Q++11 dLe ++ DFW++ p++p +vD r
QVLRVLAKEKQLSLLGDLEGGLKPQKVDFWRG---PARRPSLPPVDMR 83

VpaediqavksfleqsgIhyevlIeDVqellLeeqf<-* (SEQ ID NO: 6)
Vp+++ ++k+ Le++g+ Y++I D q+1L+e++
Fbh23565f1 41 VPFSELKDIKAYLESHGLAYSIMIKDIQVLLDEER 118

Fig. 3